

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and
Amino Acid Sequence (SEQ ID NO: 2)
5 (Acp-96614-a1)
(CD20RP2)

1	TTCCAGTGCCTCAGGCAGCCTCAGCACAAAGAAAAGAACATGGCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTCAAATTATCACCGACACCACATGGATTCAAGCACCACAG	120
1	M D S S T A H S	8
121	TCCGGTGTCTGGTATTCCTCCAGAAAATCACTGCTTCAGAAATATGAGTCCACAGAAC	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGGCCAGCACCTTCAACTCAAAGCCCCCTGCAAAAATTATTTGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCTGTTGGAAATTATGACCTTCTTTGGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTTCACTTTGTTAAAACCATATCCAAGGTTCCCTTATATTCTTTCAAGGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTGTCATTAATTCTGGAGCCTTCTAATTGCACTGAAAAGAAA	420
89	F W G S V T L F I N S G A F L I A V K R K	108
421	AACACACAGAAAACTCTGATAATTGAGCGGAATATGAATTCTTAGTGCCTGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTCTCCTCACATTGGTTCTAGATCAAAACTACATTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C C G	148
541	TTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTGGAAATTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGTGACTTCAGCATTATTGAATTATTCAATTCTCTGCCTTCTCAATTGGG	660
169	T T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATTGGTTGACTGACTGTGAGAATAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAAATCTAAAAAAAAAAAAAAAAAAAAA	760

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and
Amino Acid Sequence (SEQ ID NO: 4)
(Ajp-69406-al)
(CD20RP1)

5	1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
10	61	GCCACAGCACACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC 1 M L L Q S	120 5
15	121	CAAACCATGGGGTTCTCACAGCTTACACCAAAGGGCATCACTATCCCTCAAAGAGA 6 Q T M G V S H S F T P K G I T I P Q R E	180 25
20	181	GAAACCTGGACACATGTACCAAAAGGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC 26 K P G H M Y Q N E D Y L Q N G L P T E T	240 45
25	241	CACCGTTCTGGACTGTCCAGATCTGTGTTGCTGTGATTTCAGTCTGGGGGCCAT 46 T V L G T V Q I L C C L L I S S L G A I	300 65
30	301	CTTGGTTTTGCTCCCTACCCCTCCACATTCATCCAGCAATTCCACCTTGATGTC 66 L V F A P Y P S H F N P A I S T T L M S	360 85
35	361	TGGGTACCCATTAGGAGCTGTGTTGCGATTACTGGATCCCTCTCAATTATCTC 86 G Y P F L G A L C F G I T G S L S I I S	420 105
40	421	TGGAAAACAATCAACTAACGCCCTTGACCTGAGCAGCTTGACCTCAAATGCACTGAGTTC 106 G K Q S T K P F D L S S L T S N A V S S	480 125
45	481	TGTTACTGCAAGGAGCAGGCCCTTCTCTCTGTGACAGCATGGTAGCCCTGAGGACTGC 126 V T A G A G L F L L A D S M V A L R T A	540 145
50	541	CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCATTGGAGTACTA 146 S Q H C G S E M D Y L S S L P Y S E Y Y	600 165
55	601	TTATCCAAATAATGAAATCAAAAGATTGTCTCCGTACCCAGTGTCAAGTTAACAGGGTGCCT 166 Y P I K D C L L T S V S L T G V L	660 185
60	661	AGTGGTGTGATGCTCATCTCACTGTGGAGCTTATTAGCTGACATGCTGCTTCTGCTT 186 V V M L I F T V L E L L A A Y S S V F	720 205
65	721	TTGGTGGAAACAGCTCTACTCCAACAACCCCTGGGAGGTTCATTTCTCGACCCAGTCACA 206 W W K Q L Y S N N P G S S F S S T Q S Q	780 225
70	781	AGATCATATCCAACAGGTCAAAAGAGTCTTCACGGCTTGATATAAGTAACTCTGG 226 D H I Q Q V K K S S S R S W I *	840 241
75	841	CCTCAGAGGAAGGAAAAGCAACTCAACACTCATGGTCAAGTGTGATTAGACTTCTGAA	900
80	901	ATCTCTGCCATTAGATACTGTGAAACAAACTAAAAAAAAAGCTTTGTTGTATT	960
85	961	AAAAAAAAAAAAAAA 982	

Figure 3